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## Research Notes : Genetic linkage analysis

T. E. Devine

*Cell Culture and Nitrogen Fixation Laboratory*

B. H. Breithaupt

*Cell Culture and Nitrogen Fixation Laboratory*

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CELL CULTURE AND NITROGEN FIXATION LABORATORY  
BELTSVILLE AGRICULTURAL RESEARCH CENTER  
Beltsville, Maryland 20705

# 1) Genetic linkage analysis

The  $Rj_2$  gene (Caldwell, 1966), which conditions ineffective nodulation with strains of the cl and l22 serogroup of *Rhizobium japonicum* (Kirchner) Buhanan, and the  $Rj_4$  gene (Vest and Caldwell, 1972), conditioning an ineffective nodulation response with rhizobial strain 61 of the Beltsville Culture Collection *R. japonicum*, were tested for linkage association with the gene  $L_1$  (black pod). The  $rj_1$  gene (Williams and Lynch, 1954), conditioning a non-nodulating response with a broad spectrum of strains of *R. japonicum*, was tested for linkage with the gene  $fr$  (roots nonfluorescent in UV light) and  $L_1$  (black pod). The gene  $y_9$  (chlorophyll defective) was tested for possible linkage with the genes  $ln$  (narrow leaf), and  $P_1$  (glabrous). The  $P_1$  gene was also tested for linkage with the gene  $fr$ .

Materials and Methods. Genetic stocks (T lines) and Clark  $rj_1$   $rj_1$  were obtained from the Soybean Genetic Type Collection (Bernard and Weiss, 1973). Crosses were made in the field (Table 1) and  $F_1$  seed were advanced to the  $F_2$  generation in the greenhouse. In some crosses, the  $F_2$  progeny were assayed directly for expression of the pertinent phenotype. In other crosses, the  $F_3$  progeny were assayed and the  $F_2$  genotype rationalized from the  $F_3$  phenotypes.  $F_3$  seed was produced in the field at Beltsville. Crosses with the  $Rj_2$  and  $Rj_4$  genes were evaluated in plastic growth tray assemblies (Devine and Reisinger, 1978) and inoculated with 7-day-old broth cultures of strain 7 of *R. japonicum* from the Beltsville Culture Collection to define for  $Rj_2$  and strain 61 to define for  $Rj_4$ .

The progeny of crosses T135 x T109 and T135 x T145 were evaluated for chlorosis, narrow leaf and glabrous traits in the  $F_2$  generation in the field at Beltsville. In the case of the T215 x 'Clark'  $rj_1$  cross, each  $F_3$  seed lot was divided between two packets and two 10-foot-row plantings were made in the field. The first planting was dug and the  $F_3$  plants were scored for nodulation response to determine the presence of the  $rj_1$  gene. The field had been used for soybean cultivation for many years previously and contained abundant *R. japonicum*. The second planting was allowed to mature and the progeny rows were scored for segregation of the black pod trait.

In the cross T145 x 'Minsoy',  $F_2$  seed were germinated in petri dishes and examined, 3 days after the beginning of water imbibition, under UV light for fluorescence of the radical. After classification for fluorescence, the seedlings were transplanted into rows in growth trays, cultured in a growth room, and classified for the glabrous character at the first trifoliolate-leaf stage. For the cross of Clark  $rj_1$  x Minsoy,  $F_2$  seedlings were classified for fluorescence as previously described, then were inoculated with strain 7 of *R. japonicum* and transplanted into rows in vermiculite-filled growth trays. After an additional 3 weeks growth, the seedlings were removed from the vermiculite and classified for nodulation response.

In the cross T215 x 'Hardee', each  $F_3$  seed lot was divided and about 50 seed were evaluated for the presence of the nodulation response gene  $Rj_2$  under conditions of controlled inoculation with rhizobial strain 7 in growth trays in the greenhouse. The remaining seed was planted in 10-foot rows in

the field at Beltsville, MD, and grown to maturity when rows were classified for segregation for the black pod trait. Similarly, in the 'Hill' x T215 cross, the  $F_3$  seed lots were divided and one portion of seed was characterized for the black pod trait in the field and the other portion was characterized for the  $Rj_4$  nodulation response gene in growth trays after inoculation with rhizobial strain 61.

**Results.** Results of the seven linkage tests are given in Table 2. All of the traits tested displayed independent assortment indicating they were not genetically linked to the genes tested.

Table 1.

Cross	Generation of progeny evaluated	Trait characterized		
		In field	In growth trays	In petri dishes
T135 ( $y_9$ LN) x T109 ( $y_9$ ln)	$F_2$	$y_9$ ln	--	--
T135 ( $y_9 p_1$ ) x T124 ( $y_9 P_1$ )	$F_2$	$y_9$ $p_1$	--	--
T215 ( $L_1$ $Rj_1$ ) x Clark $rj_1$ ( $l_1 rj_1$ )	$F_3$	$l_1$ $rj_1$	--	--
T145 ( $Fr$ $P_1$ ) x Minsoy ( $fr$ $p_1$ )	$F_2$	--	$p_1$	$fr$
Clark $rj_1$ ( $rj_1$ $Fr$ ) x Minsoy ( $Rj_1$ $fr$ )	$F_2$	--	$rj_1$	$fr$
T215 ( $L_1$ $rj_2$ ) x Hardee ( $l_1$ $Rj_2$ )	$F_3$	$L_1$	$rj_2$	--
Hill ( $Rj_4$ $l_1$ ) x T215 ( $rj_4$ $L_1$ )	$F_3$	$L_1$	$rj_4$	--



Table 2. Soybean genetic linkage tests

Genes	a	b	c	d	Sum	%R*	SE	Phase
T135 ( $y_9 y_9 Ln Ln$ ) x T109 ( $Y_9 Y_9 ln ln$ )								
$Y_9 y_9 Ln ln$	171	45	52	14	282	50	4	R
T215 ( $L_1 L_1 rj_2 rj_2$ ) x Hardee ( $l_1 l_1 Rj_2 Rj_2$ )								
$L_1 l_1 Rj_2 rj_2$	55	11	20	6	92	55	7	R
Hill ( $Rj_4 Rj_4 l_1 l_1$ ) x T215 ( $rj_4 rj_4 L_1 L_1$ )								
$Rj_4 rj_4 L_1 l_1$	132	34	27	5	198	45	6	R
T135 ( $y_9 y_9 P_1 P_1$ ) x T145 ( $Y_9 Y_9 P_1 P_1$ )								
$Y_9 y_9 P_1 P_1$	144	40	55	17	256	49	5	C
T145 ( $P_1 P_1 Fr Fr$ ) x Minsoy ( $p_1 p_1 fr fr$ )								
$P_1 p_1 Fr fr$	291	91	102	32	516	50	3	C
Clark $rj_1$ ( $rj_1 rj_1 Fr Fr$ ) x Minsoy ( $Rj_1 Rj_1 fr fr$ )								
$Rj_1 rj_1 Fr fr$	76	31	24	10	141	50	6	R
T215 ( $L_1 L_1 Rj_1 Rj_1$ ) x Clark $rj_1$ ( $l_1 l_1 rj_1 rj_1$ )								
$L_1 l_1 Rj_1 rj_1$	115	31	44	14	204	48	5	R

\*Recombination percentages calculated by the product method (Immer and Henderson, 1943).

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T. E. Devine  
B. H. Breithaupt